

Serial No. 09/807,946
Amendment Dated January 18, 2007
Reply to Office Action of October 18, 2006
APPENDIX B – Sequence Analyses showing conserved domains, motifs, amino acids

PILEUP Multiple Sequence Alignment

Symbol comparison table: blosum62.cmp CompCheck: 1102

GapWeight: 8 GapLengthWeight: 2

BB1410SID4_pileup_121608.txt MSF: 351 Type: P January 5, 2007 10:34
Check: 7274 ..

BB1410SID6	p0016.ctsas50r corn EST (ELECTED sequence)
BB1410sid8	p0016.ctsas50r corn FIS (ELECTED sequence)
BB1410sid16	scr1c.pk001.d2/ses4d.pk0033.c8 contig soy clones
BB1410sid18	scr1c.pk001.d2 soy FIS
BB1410sid20	ses4d.pk0033.c8 soy FIS/CGS
BB1410sid12	p0083.cldev71r corn EST
BB1410sid14	p0083.cldev71r corn FIS
BB1410SID4	cpilc.pk012.p19 corn FIS/CGS
BB1410sid2	cpglc.pk006.b16/cpilc.pk012.p19 contig corn clones
BB1410sid22	sgs5c.pk0002.f2 soy CGS
BB1410sid24	ssm.pk0060.h4 FIS/NCBI GI#4395781 contig
BB1410sid25	A. thaliani NCBI GI#4090200
BB1410sid10	p0058.chpab57r corn FIS/CGS

FORMATTING to identify conserved regions &/or residues:

Identical or conservative aa residues as compared to SEQ ID NOs: 6&8
shown in **BOLD** & **Shaded**; Homeobox domain **boxed**

Conservative aa substitutions: McKay *et al.* (1996) Genomics 36:305-315.
See Figure 2 legend – (P, A, G, S, T); (E, D, N, Q); (V, I, L, M); (F, W, Y); (R, K, H)

	1				50
BB1410SID6	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid8	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid16	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid18	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid20	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid12	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid14	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410SID4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid22	MKVHQFARG.	FWEHEPSLTL	GCKRLRPLAP	KLSNTDTISP	PHHPVTTFDL
BB1410sid24	MKVHQFTRGL	IWEHEPFLTL	GCKRLRPLAP	KLPNTKTITT	P.....FDL
BB1410sid25	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid10	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

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	51				100
BB1410SID6	~~~~~	~~MAANAGGG	GAGGGSGSGS	VAAPAVCRPS	GSRWTPTPEQ
BB1410sid8	~~~~~	~~MAANAGGG	GAGGGSGSGS	VAAPAVCRPS	GSRWTPTPEQ
BB1410sid16	~~~~~	~~~~~MESS	HSTAEDESGW	KGSSGAH.SS	VSRWSPTKEQ
BB1410sid18	~~~~~	~~~~~S	HSTAEDESGW	KGSSGAH.SS	VSRWSPTKEQ
BB1410sid20	~~~~~	~~~~~MESH	SSDAEAE...	..NVRTH.SS	VSRWSPTKEQ
BB1410sid12	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~Q
BB1410sid14	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~WATKEQ
BB1410SID4	~~~~~	~~~~~	~~~~~MEAL	SGRVGVKC..	.GRWNPTAEQ
BB1410sid2	~~~~~	~~~~~	~~~~~MEAL	SGRVGVKC..	.GRWNPTAEQ
BB1410sid22	KSFIKPESAS	RKLGIGSSDD	NTNKRDPSSP	QGOAETHIPG	GTRWNPTQEQ
BB1410sid24	KSFIKPESGP	RK..PVSSDD	..TKKDPSP	QGOIETH.PG	GTRWNPTQEQ
BB1410sid25	~~~~~MEPPQ	HQH HHHQADQ	ESGNNNNKSG	SGGYTCRQTS	.TRWTPTTEQ
BB1410sid10	~~~~~	~~~~~	~~~~~MEGGLS	PERHAAAEPV	RSRWTPKPEQ
	101				150
BB1410SID6	IRMLKELYYG	CGIRSPSSEQ	IQRITAMLRQ	HGKIEGKNVF	YWFQNHKARE
BB1410sid8	IRMLKELYYG	CGIRSPSSEQ	IQRITAMLRQ	HGKIEGKNVF	YWFQNHKARE
BB1410sid16	IDMLENF.YK	QGIRTPSTEQ	IQOITSRLRA	YGYIEGKNVF	YWFQNHKARQ
BB1410sid18	IDMLENF.YK	QGIRTPSTEQ	IQOITSRLRA	YGYIEGKNVF	YWFQNHKARQ
BB1410sid20	IDMLENL.YK	QGIRTPSTEQ	IQOITSRLRA	YGHIEGKNVF	YWFQNHKARQ
BB1410sid12	VAVLEGL.YE	HGLRTPSAEQ	IQOITGRLRE	HGAIEGKNVF	YWFQNHKARQ
BB1410sid14	VAVLEGL.YE	HGLRTPSAEQ	IQOITGRLRE	HGAIEGKNVF	YWFQNHKARQ
BB1410SID4	VKVLTEL.FR	AGLRTPSTEQ	IQRISTHLSA	FGKVESKNVF	YWFQNHKARE
BB1410sid2	VKVLTEL.FR	AGLRTPSTEQ	IQRISNQLSA	FGKGENKNVL	LTGPKQKGRE
BB1410sid22	IGILEML.YR	GGMRTPNAAQ	IEQITAQLSK	YGKIEGKNVF	YWFQNHKARE
BB1410sid24	IGILEML.YK	GGMRTPNAAQ	IEQITVOLGK	YGKIEGKNVF	YWFQNHKARE
BB1410sid25	IKILKELYYN	NAIRSPTADQ	IQKITARLRQ	FGKIEGKNVF	YWFQNHKARE
BB1410sid10	ILILESI.FN	SGMVNPPKDE	TVRIRKLLER	FGAVGDANVF	YWFQNRRSRS
	151				200
BB1410SID6	RQKRRLTSLD	VNVPAAGAAD	ATTSQLGVLS	LSSPPPSGA.	APPS..PTLG
BB1410sid8	RQKRRLTSLD	VNVPAAGAAD	ATTSQLGVLS	LSSPPPSGA.	APPS..PTLG
BB1410sid16	RQKLKQKQOS	IAYCNC..FL	HASHPICQNV	VCVHIVCKR.	VDSAFILTNO
BB1410sid18	RQKLKQKQOS	IAYCNC..FL	HASHPICQNV	VCAPYCLQK.	SGFSFYPHQP
BB1410sid20	RQKL.MKQQT	IAYSNR..FL	RASHPICQNV	ACAPYCLQR.	SGFSFYPOQS
BB1410sid12	RQX..QXAGQ	L....R..LL	QQAPP.PA..	.PAAARALH.	APRATVPSRP
BB1410sid14	RQR..QKQDS	FAYFSR..LL	RRPPPLPVLS	MPPAPPYHH.	ARVPAPPAIP
BB1410SID4	RHHHKRRRG	ASSSSPDGSGS	GRGSNNEEDG	RGAASQSHD.	ADDADLVLPQ
BB1410sid2	RQQKKR~~~	~~~~~	~~~~~	~~~~~	~~~~~
BB1410sid22	RQKQKRNNLG	LAHSPRTTLT	TSPPFSCCV.	ITTMDDTTKRG
BB1410sid24	RQKQKRSSLA	SSHSPRTPTI	HS.....	VVTLETT.RG
BB1410sid25	RQKKRFNGTN	MTTPSSSP..	.NSVMAAND	HYHPLLHHH.	HGVEMQRPAN
BB1410sid10	RRRORQLAQ	AAASSSSSGS	PPTSGIAPGH	ATASSTAGMF	AHGATYGSSA

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201
BB1410SID6 LYAAGNGGGS AVLLDTSSDW GSSGAAMATE TCFLQVGAVV RSFLGHCAQF
BB1410sid8 FYAAGNGGGS AVLLDTSSDW GSSGAAMATE TCFLQVGAVV RSFLGHCAQF
BB1410sid16 RCLQV~~~~~
BB1410sid18 KVLASVGISS RIETGSFGML RICDGMQ.SE HPDYNYSTSN REALTLFPLH
BB1410sid20 KVLASGGISS ...TGPLGMQ RMFDGMQSSE HPD.....CN REVLTFLFPLH
BB1410sid12 RP~~~~~
BB1410sid14 MPMAPPPPAA CNDNGGARVI YRNPFIYVAA QAPPANAAAY YPQQQQQQQ
BB1410SID4 PESKREARSY GHHRRLVTCY VRDVVEQQEA SPSWERPTRE VETLELFPLK
BB1410sid2 ~~~~~
BB1410sid22 EVVERE.EED SPL.KKCRSW AFEYLEDQ.. ....RE..EE HRTLELFPLH
BB1410sid24 EVVERDHEED SPYKKKCRWW VFDCLEEQNM SSPCEQ..EE HRTLELFPLH
BB1410sid25 SVNVLNODH HLYHHNKPPY SFNNGNLNHA SSGTECGVNV ASNGYMSSHV
BB1410sid10 SASWPPPPSC EGMMGDLDYG GGDDLFAISR QMGYASGGGS GSASSAAVAH

251
BB1410SID6 HVRTYELIAA SFHPPVYITV RYGGARPQDY MGVTDTGSSS QWPRFSSSDT
BB1410sid8 HVRTYELIAA SFHPPVYITV RYGGARPQDY MGVTDTGSSS QWPRFASSDT
BB1410sid16 ~~~~~
BB1410sid18 PTGILEEKTTHHSVDVTDKSFVSIADVENGHLGNQPCFNFQY~~~~~
BB1410sid20 PTGILKEKTTHQVPSLASTSVV..AVDEDGHLGNQPFNF FTTEPRSRE~
BB1410sid12 ~~~~~
BB1410sid14 QVTVMYQYPR MEVAGQDKMM TRAAAHQOO HNGAGQPPGR AGHPSRETLO
BB1410SID4 SYGDLEAAEK VRSYVRGIAA TSEQCRELSF FDVSAGRDP LELRLCSFGP
BB1410sid2 ~~~~~
BB1410sid22 PEGR~~~~~
BB1410sid24 PEGR~~~~~
BB1410sid25 YGSMEQDCSM NYNNVGGGWA NMDHHYSSAP YNFFDRAKPL FGLEGHQDEE
BB1410sid10 HEQQQQLYYS PCQPASMTVF INGVA TEVPR GPIDLRSMFG QDVMLVHSTA

301
BB1410SID6 IMA~~~~~
BB1410sid8 IM~~~~~
BB1410sid16 ~~~~~
BB1410sid18 ~~~~~
BB1410sid20 ~~~~~
BB1410sid12 ~~~~~
BB1410sid14 LFPPPAHLRA AARQGARRQR Q~~~~~
BB1410SID4 ~~~~~
BB1410sid2 ~~~~~
BB1410sid22 ~~~~~
BB1410sid24 ~~~~~
BB1410sid25 ECGGDAYLEH RRTLPLFPMH GEDHINGGSG AIWKYQSEV RPCASLELRL
BB1410sid10 GLLPVNEYGV LTQSLQMGES YFLVTRGY~

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351
BB1410SID6 ~
BB1410sid8 ~
BB1410sid16 ~
BB1410sid18 ~
BB1410sid20 ~
BB1410sid12 ~
BB1410sid14 ~
BB1410SID4 ~
BB1410sid2 ~
BB1410sid22 ~
BB1410sid24 ~
BB1410sid25 N
BB1410sid10 ~

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Query: BB1410SID6 from: 1 to: 238

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	---
Homeobox	Homeobox domain	46.8	5e-10	1

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Homeobox	1/1	28	90 ..	1	57 []	46.8	5e-10

Homeobox: domain 1 of 1, from 28 to 90: score 46.8, E = 5e-10

```

      *->rrkRTtftpeQleeLEkeFqk..nrYPsreeReeLAkkL....gLte
      +R+t+tpeQ++ L++++ + r Ps+e+++++ ++L+++++++
BB1410SID6      28      SGRWTPPTPEQIRMLKELYGcgIRSPSSEQIQRITAMlrqhgKIEG 74

      rqVkvWFQNRRaKwKk<-*
      ++V++WFQN++a++++
BB1410SID6      75 KNVFYWFQNHKARERQ      90

```

Query: BB1410SID8 from: 1 to: 237

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	---
Homeobox	Homeobox domain	46.8	5e-10	1

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Homeobox	1/1	28	90 ..	1	57 []	46.8	5e-10

Homeobox: domain 1 of 1, from 28 to 90: score 46.8, E = 5e-10

```

      *->rrkRTtftpeQleeLEkeFqk..nrYPsreeReeLAkkL....gLte
      +R+t+tpeQ++ L++++ + r Ps+e+++++ ++L+++++++
BB1410SID8      28      SGRWTPPTPEQIRMLKELYGcgIRSPSSEQIQRITAMlrqhgKIEG 74

      rqVkvWFQNRRaKwKk<-*
      ++V++WFQN++a++++
BB1410SID8      75 KNVFYWFQNHKARERQ      90

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Query: BB1410SID25 from: 1 to: 291 A. thaliani GI 4090200
 Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Homeobox	Homeobox domain	44.3	2.7e-09	1
RMMBL	RNA-metabolising metallo- β -lactamase	-5.2	10	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Homeobox	1/1	34	96	..	1 57 []	44.3	2.7e-09

Alignments of top-scoring domains:

Homeobox: domain 1 of 1, from 34 to 96: score 44.3, E = 2.7e-09

```

      *->rrkRTtftpeQleeLEkeFqk..nrYPsreeReeLAkkL....gLte
      +R+t+t+eQ+++L+++ + r P+++++++ ++L++ ++++
BB1410SID2    34    TSTRWTPTEQIKILKELYNNaIRSPTADQIQKITARLrqfgKIEG 80

      rqVkvWFQNRaKwKk<-*
      ++V++WFQN++a++++
BB1410SID2    81 KNVFYWFQNHKARERQ      96
  
```